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RAW SEQUENCE LISTING

DATE: 05/06/2002

PATENT APPLICATION: US/10/047,539

TIME: 13:52:11

Input Set : A:\Vos27.app

Output Set: N:\CRF3\05062002\J047539.raw

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3 <110> APPLICANT: MOLLING, KARIN
4     PAVLOVIC, JOVAN
5     NAWRATH, MICHAEL
7 <120> TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING
8     CANCER
10 <130> FILE REFERENCE: VOS-27
12 <140> CURRENT APPLICATION NUMBER: 10/047,539
13 <141> CURRENT FILING DATE: 2002-01-15
15 <150> PRIOR APPLICATION NUMBER: EP 01 10 0914.9
16 <151> PRIOR FILING DATE: 2001-01-16
18 <160> NUMBER OF SEQ ID NOS: 13
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1881
24 <212> TYPE: DNA
25 <213> ORGANISM: Mus musculus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(1881)
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33 Met Val Gly Val Gln Arg Arg Ser Phe Leu Pro Val Leu Val Leu Ser
34   1             5             10             15
36 gct ctg ctg gct gtg ggg gcc cta gaa gga tcc agg aat cag gac tgg   96
37 Ala Leu Leu Ala Val Gly Ala Leu Glu Gly Ser Arg Asn Gln Asp Trp
38             20             25             30
40 ctt ggt gtc cca aga caa ctt gta act aaa acc tgg aac agg cag ctg   144
41 Leu Gly Val Pro Arg Gln Leu Val Thr Lys Thr Trp Asn Arg Gln Leu
42             35             40             45
44 tac ccc gag tgg aca gag gtg cag ggg tct aac tgc tgg aga ggt ggc   192
45 Tyr Pro Glu Trp Thr Glu Val Gln Gly Ser Asn Cys Trp Arg Gly Gly
46             50             55             60
48 cag gta tct ctg agg gtc att aat gat ggg cct aca ctg gtt ggt gca   240
49 Gln Val Ser Leu Arg Val Ile Asn Asp Gly Pro Thr Leu Val Gly Ala
50   65             70             75             80
52 aat gcc tcc ttt tcc att gcc ctg cac ttc cct gga agt caa aag gta   288
53 Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Gly Ser Gln Lys Val
54             85             90             95
56 cta ccg gat ggt cag gtt atc tgg gcc aac aac acc atc atc aat ggg   336
57 Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly
58             100            105            110
60 agc cag gtg tgg gga gga cag cca gtg tat cca cag gag cct gat gat   384
61 Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Pro Asp Asp

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| | | | | |
|-----|---|------|-----|-----|
| 62 | 115 | 120 | 125 | |
| 64 | gcc tgt gtc ttc cct gac ggt gga ccc tgc cca tct ggt cct aaa cct | 432 | | |
| 65 | Ala Cys Val Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Pro Lys Pro | | | |
| 66 | 130 | 135 | 140 | |
| 68 | ccg aag aga agc ttt gtt tat gtt tgg aag acc tgg gga aaa tac tgg | 480 | | |
| 69 | Pro Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Lys Tyr Trp | | | |
| 70 | 145 | 150 | 155 | 160 |
| 72 | caa gtt ctg ggg ggt cca gtg tcc agg tgc agc att gct acg cgc cac | 528 | | |
| 73 | Gln Val Leu Gly Gly Pro Val Ser Arg Ser Ser Ile Ala Thr Arg His | | | |
| 74 | 165 | 170 | 175 | |
| 76 | gca aag ctg ggc aca cac aca atg gaa gtg act gtc tac cac cga cgg | 576 | | |
| 77 | Ala Lys Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg | | | |
| 78 | 180 | 185 | 190 | |
| 80 | ggt tcc cag agc tac gtg ccc ctt gct cac gcc agt tca acc ttc acc | 624 | | |
| 81 | Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ala Ser Ser Thr Phe Thr | | | |
| 82 | 195 | 200 | 205 | |
| 84 | att act gac cag gta cct ttc tcc gtg agt gtg tcc cag cta cag gcc | 672 | | |
| 85 | Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala | | | |
| 86 | 210 | 215 | 220 | |
| 88 | ttg gac gga gag acc aag cac ttc ctg aga aat cat cct ctc atc ttt | 720 | | |
| 89 | Leu Asp Gly Glu Thr Lys His Phe Leu Arg Asn His Pro Leu Ile Phe | | | |
| 90 | 225 | 230 | 235 | 240 |
| 92 | gcc ctt cag ctc cac gac ccc agt ggt tat ttg gcc gag gcc gac ctc | 768 | | |
| 93 | Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu | | | |
| 94 | 245 | 250 | 255 | |
| 96 | tcc tac aca tgg gac ttt gga gat ggt act ggg acc ctg atc tct cgg | 816 | | |
| 97 | Ser Tyr Thr Trp Asp Phe Gly Asp Gly Thr Gly Thr Leu Ile Ser Arg | | | |
| 98 | 260 | 265 | 270 | |
| 100 | gca ctt gat gtc act cac act tac ctg gag tgc ggc tca gtc act gcc | 864 | | |
| 101 | Ala Leu Asp Val Thr His Thr Tyr Leu Glu Ser Gly Ser Val Thr Ala | | | |
| 102 | 275 | 280 | 285 | |
| 104 | cag gtg gta ctg cag gct gcc att cct ctt gtt tcc tgt ggt tcc tcc | 912 | | |
| 105 | Gln Val Val Leu Gln Ala Ala Ile Pro Leu Val Ser Cys Gly Ser Ser | | | |
| 106 | 290 | 295 | 300 | |
| 108 | cca gtc ccg ggt acc aca gat ggc tac atg cca act gca gaa gca cct | 960 | | |
| 109 | Pro Val Pro Gly Thr Thr Asp Gly Tyr Met Pro Thr Ala Glu Ala Pro | | | |
| 110 | 305 | 310 | 315 | 320 |
| 112 | gga acc aca tct agg caa gga acc act aca aaa gtt gtg ggt act aca | 1008 | | |
| 113 | Gly Thr Thr Ser Arg Gln Gly Thr Thr Thr Lys Val Val Gly Thr Thr | | | |
| 114 | 325 | 330 | 335 | |
| 116 | cct ggc cag atg cca act aca cag ccc tct gga acc aca gtt gta caa | 1056 | | |
| 117 | Pro Gly Gln Met Pro Thr Thr Gln Pro Ser Gly Thr Thr Val Val Gln | | | |
| 118 | 340 | 345 | 350 | |
| 120 | atg cca acc aca gag gtc aca gct act aca tct gag cag atg ctg acc | 1104 | | |
| 121 | Met Pro Thr Thr Glu Val Thr Ala Thr Thr Ser Glu Gln Met Leu Thr | | | |
| 122 | 355 | 360 | 365 | |
| 124 | tca gcg gtc ata gat acc aca ctg gca gag gtg tca act aca gag ggt | 1152 | | |
| 125 | Ser Ala Val Ile Asp Thr Thr Leu Ala Glu Val Ser Thr Thr Glu Gly | | | |
| 126 | 370 | 375 | 380 | |

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128 aca ggt acc aca ccc aca agg cct tct gga acc acc gtt gca caa gca 1200
129 Thr Gly Thr Thr Pro Thr Arg Pro Ser Gly Thr Thr Val Ala Gln Ala
130 385 390 395 400
132 aca acc aca gag ggt cca gat gcc agc cca ttg ctg ccc aca caa agt 1248
133 Thr Thr Thr Glu Gly Pro Asp Ala Ser Pro Leu Leu Pro Thr Gln Ser
134 405 410 415
136 tct aca ggg tcc att agc cct cta ctg gat gac acc gac acc ata atg 1296
137 Ser Thr Gly Ser Ile Ser Pro Leu Leu Asp Asp Thr Asp Thr Ile Met
138 420 425 430
140 ctt gtg aag aga caa gtt ccc ctg gac tgt gtt cta tat cga tat ggt 1344
141 Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr Gly
142 435 440 445
144 tct ttc tcc ctc gcc ctg gac att gtc cag ggt att gaa agt gct gag 1392
145 Ser Phe Ser Leu Ala Leu Asp Ile Val Gln Gly Ile Glu Ser Ala Glu
146 450 455 460
148 atc ctg cag gct gtg cca ttc agt gaa ggg gat gca ttt gag ctg act 1440
149 Ile Leu Gln Ala Val Pro Phe Ser Glu Gly Asp Ala Phe Glu Leu Thr
150 465 470 475 480
152 gtg tcc tgc caa ggc ggg cta ccc aag gaa gcc tgt atg gac att tca 1488
153 Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Asp Ile Ser
154 485 490 495
156 tca cca ggg tgc cag ccc cct gcc cag agg ctg tgc cag tct gtt cca 1536
157 Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Ser Val Pro
158 500 505 510
160 ccg agc cca gac tgc cag ctg gtt cta cac caa gtg ctg aaa ggt ggc 1584
161 Pro Ser Pro Asp Cys Gln Leu Val Leu His Gln Val Leu Lys Gly Gly
162 515 520 525
164 tca ggg aca tat tgc ctc aat gtg tct ttg gct gac gcc aac agc ctg 1632
165 Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala Asn Ser Leu
166 530 535 540
168 gca gtg gcc agc acc caa ctt gtt gtt cct ggt caa gac ggt ggc ctt 1680
169 Ala Val Ala Ser Thr Gln Leu Val Val Pro Gly Gln Asp Gly Gly Leu
170 545 550 555 560
172 ggg cag gct ccc ttg ctt gta ggt atc ttg ctg gtg ttg gtg gct gtg 1728
173 Gly Gln Ala Pro Leu Leu Val Gly Ile Leu Leu Val Leu Val Ala Val
174 565 570 575
176 gtc ctt gca tct ctg ata cta ggc ata gac tta aga agc agg gct cag 1776
177 Val Leu Ala Ser Leu Ile Leu Gly Ile Asp Leu Arg Ser Arg Ala Gln
178 580 585 590
180 ttt ccc aaa tgc cac atg gta gca ctc act gct gcg cct gcc tcc ggt 1824
181 Phe Pro Lys Cys His Met Val Ala Leu Thr Ala Ala Pro Ala Ser Gly
182 595 600 605
184 ctt cgc gcc cgc ggc ctt gga gaa aac agc ccg ctc ctc agt gga cag 1872
185 Leu Arg Ala Arg Gly Leu Gly Glu Asn Ser Pro Leu Leu Ser Gly Gln
186 610 615 620
188 cag gtc tga 1881
189 Gln Val
190 625
193 <210> SEQ ID NO: 2

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194 <211> LENGTH: 626
195 <212> TYPE: PRT
196 <213> ORGANISM: Mus musculus
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203          20          25          30
205 Leu Gly Val Pro Arg Gln Leu Val Thr Lys Thr Trp Asn Arg Gln Leu
206          35          40          45
208 Tyr Pro Glu Trp Thr Glu Val Gln Gly Ser Asn Cys Trp Arg Gly Gly
209          50          55          60
211 Gln Val Ser Leu Arg Val Ile Asn Asp Gly Pro Thr Leu Val Gly Ala
212  65          70          75          80
214 Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Gly Ser Gln Lys Val
215          85          90          95
217 Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly
218          100         105         110
220 Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Pro Asp Asp
221          115         120         125
223 Ala Cys Val Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Pro Lys Pro
224          130         135         140
226 Pro Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Lys Tyr Trp
227 145          150         155         160
229 Gln Val Leu Gly Gly Pro Val Ser Arg Ser Ser Ile Ala Thr Arg His
230          165         170         175
232 Ala Lys Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg
233          180         185         190
235 Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ala Ser Ser Thr Phe Thr
236          195         200         205
238 Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala
239          210         215         220
241 Leu Asp Gly Glu Thr Lys His Phe Leu Arg Asn His Pro Leu Ile Phe
242 225          230         235         240
244 Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu
245          245         250         255
247 Ser Tyr Thr Trp Asp Phe Gly Asp Gly Thr Gly Thr Leu Ile Ser Arg
248          260         265         270
250 Ala Leu Asp Val Thr His Thr Tyr Leu Glu Ser Gly Ser Val Thr Ala
251          275         280         285
253 Gln Val Val Leu Gln Ala Ala Ile Pro Leu Val Ser Cys Gly Ser Ser
254          290         295         300
256 Pro Val Pro Gly Thr Thr Asp Gly Tyr Met Pro Thr Ala Glu Ala Pro
257 305          310         315         320
259 Gly Thr Thr Ser Arg Gln Gly Thr Thr Thr Lys Val Val Gly Thr Thr
260          325         330         335
262 Pro Gly Gln Met Pro Thr Thr Gln Pro Ser Gly Thr Thr Val Val Gln
263          340         345         350
265 Met Pro Thr Thr Glu Val Thr Ala Thr Thr Ser Glu Gln Met Leu Thr

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266          355          360          365
268 Ser Ala Val Ile Asp Thr Thr Leu Ala Glu Val Ser Thr Thr Glu Gly
269          370          375          380
271 Thr Gly Thr Thr Pro Thr Arg Pro Ser Gly Thr Thr Val Ala Gln Ala
272 385          390          395          400
274 Thr Thr Thr Glu Gly Pro Asp Ala Ser Pro Leu Leu Pro Thr Gln Ser
275          405          410          415
277 Ser Thr Gly Ser Ile Ser Pro Leu Leu Asp Asp Thr Asp Thr Ile Met
278          420          425          430
280 Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr Gly
281          435          440          445
283 Ser Phe Ser Leu Ala Leu Asp Ile Val Gln Gly Ile Glu Ser Ala Glu
284          450          455          460
286 Ile Leu Gln Ala Val Pro Phe Ser Glu Gly Asp Ala Phe Glu Leu Thr
287 465          470          475          480
289 Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Asp Ile Ser
290          485          490          495
292 Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Ser Val Pro
293          500          505          510
295 Pro Ser Pro Asp Cys Gln Leu Val Leu His Gln Val Leu Lys Gly Gly
296          515          520          525
298 Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala Asn Ser Leu
299          530          535          540
301 Ala Val Ala Ser Thr Gln Leu Val Val Pro Gly Gln Asp Gly Gly Leu
302 545          550          555          560
304 Gly Gln Ala Pro Leu Leu Val Gly Ile Leu Leu Val Leu Val Ala Val
305          565          570          575
307 Val Leu Ala Ser Leu Ile Leu Gly Ile Asp Leu Arg Ser Arg Ala Gln
308          580          585          590
310 Phe Pro Lys Cys His Met Val Ala Leu Thr Ala Ala Pro Ala Ser Gly
311          595          600          605
313 Leu Arg Ala Arg Gly Leu Gly Glu Asn Ser Pro Leu Leu Ser Gly Gln
314          610          615          620
316 Gln Val
317 625
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322 <211> LENGTH: 2131
323 <212> TYPE: DNA
324 <213> ORGANISM: Homo sapiens
326 <220> FEATURE:
327 <221> NAME/KEY: CDS
328 <222> LOCATION: (12)..(2018)
330 <400> SEQUENCE: 3
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333          1          5          10
335 gtg ata ggt gct ttg ctg gct gtg ggg gct aca aaa gta ccc aga aac 98
336 Val Ile Gly Ala Leu Leu Ala Val Gly Ala Thr Lys Val Pro Arg Asn
337          15          20          25

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VERIFICATION SUMMARY

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